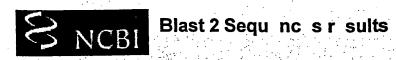
EXHIBIT 16

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing prote FEMS Microbiol Lett. 174:247-250	em and nucleotide sequences,
Program Biospin Matrix BEOSEN62	
Parameters used in <u>BLASTN</u> program only: Reward for a match: Penalty for a mismatch:	
■ Use Mega BLAST Strand option Not Applicable	
Open gap 11 and extension gap 1 penalties gap x_dropoff 50 expect 10.0 word size 3 Filter M Align	
Sequence 1 Enter accession or GI CLONED E or download from file	
or sequence in FASTA format from: 0 to: 0	
DYGNSPYESTULTHALSSOPMLSISEASUNGLRSUUMUFSGLNVPHTGWOGLWSWGWARTO DPEPASSATITDPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT KLNERYAKNNVSSKNYSCOGEMLFSLOEGFLLAKLVGLYSYGDHNCHHPYTOGENLTSQGT	
FRSQTMGGAVFFDLFMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV LVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF	and the second of the second o
Sequence 2 Enter accession or GI CT2 MURD or download from file	
or sequence in FASTA format from: 0 to: 0	
VAGLENDPVA PT7CT2	Mundin Inf. Immunit 61:4406, 1993
	61:4406, 1993
	·
Alers Sciencing	



BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Sequence 1 |cl|seq_1 | Length 955 | PRPE CLOSE | ATCC | PTA 2467 |
Sequence 2 |cl|seq_2 | Length 10 | PTTCTZ |
No significant similarity was found

This tool produces the alignment of two given sequences using BLAST engine for local alignment.

The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences",

FEMS Microbiol Lett. 174:247-250

Program Filasp Matrix BEGSUM62: Expression of the program only:

Parameters used in BLASTN program only: Reward for a match: Penalty for a mismatch:	
Use Mega BLAST Strand option Not Applicable	
Open gap 11 and extension gap 1 penalties gap x_dropoff 50 expect 10.0 word size 3 Filter	
Sequence 1 Enter accession or GI CLONED E or download from file	
or sequence in FASTA format from: 0 to: 0	
DIGNSPIESTDUTHALSSQPMLSISEASUNQLKSDUMDFSGLNVPHIGWQGLWSWGWAKTQ DPEPASSATITDPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKPSQTYT KLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCHHFYTQGENLTSQGT FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV LVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF	
Sequence 2 Enter accession or GI CT4 MURD or download from file	
or sequence in FASTA format from: 0 to: 0	
PTTSDVAGLEKDPVA PT 7 C + 4	

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequ nces results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Sequence 1 Icliseq_1 Length 955 PHPE ATCC PTA 2462

Sequence 2 lcl/seq_2 Length 15 PT 7 CH 4 No significant similarity was found

This tool produces the alignment of two given sequences using BLAST engine for local alignment. Th stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250 Program adjustices Andrew Matrix BEOSUMG Series Parameters used in **BLASTN** program only: Penalty for a mismatch: Reward for a match: Use Mega BLAST Strand option Not Applicables penalties and extension gap 1 Open gap 11 expect 10.0 word size 3 Filter 🗹 gap x_dropoff 50 Sequence 1 Enter accession or GI CLONED E or download from file or sequence in FASTA format from: 0 to: 0 DIGNSPIESTULTHALSSQFMLSISEASUNQLKSDUMDFSGFWALARAMGMAKIA DPEPASSATITDPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTFSLKFSQTYT KLNERYAKNINVSSKNYSCOGEMLFSLOEGFLLAKLVGLYSYGDHNCHHFYTQGENLTSQGT FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV LVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF Sequence 2 Enter accession or GI CT# MURD: or download from file PT7et5 or sequence in FASTA format from: 0 to: 0 PTTSDVAGLEKDPKD

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

(CleanInput)

Align



Blast 2 Sequenc s results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix BEOSUM62: gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.0 wordsize: 3 Filter Align

Sequence 2 Icl|seq_2 Length 15 PT7CT5

Sequence 1 Icl|seq_1 Length 955 PMPE ATEC PTA 2462

No significant similarity was found

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

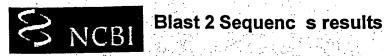
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250 Program ablasto Matrix DE6SUM62 C Parameters used in **BLASTN** program only: Reward for a match: Penalty for a mismatch: Use Mega BLAST Strand option Not Applicable Open gap 11 and extension gap 1 penalties gap x_dropoff 50 expect 10.0 word size 3 Filter 🖾 Sequence 1 Enter accession or GI CLONED E or download from file or sequence in FASTA format from: 0 to: 0 DIGNSFIESTULTHALSSUPPLSISEASUNGLRSUUPUFSGLNVFHIGWQGLWSWGWAKTQ DPEPASSATITDPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS AELTPSDHPFWGITGGGLGMMVYQEPRENHPGPHMRSSGYFAGMIAGQTHTFSLKFSQTYT KINERYAKNINVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCHHFYTQGENLTSQGT FRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV LVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF Sequence 2 Enter accession or GI CT7 MURD: or download from file or sequence in FASTA format from: 0 to: 0 p=+er7 NPASTTSDVAGLEKDPVA

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

(GlearInput)

Allign

Page: 1



BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix BI	(0SUM(62) C	gap open: 1	gap e	xtension:	1
x_dropoff:	50 expect: 10.0	wordsize: 3	Filter		918

Sequence 1 lcl|seq_1 Length 955 Sequence 2 Icl|seq_2 Length 18 No significant similarity was found

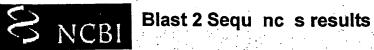
This tool produces the alignment of two given sequences using <u>BLAST</u> engine for local alignment.

The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from <u>NCBI stp site</u>

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Blasto Matrix BEOSUM67	
Parameters used in <u>BLASTN</u> program only: Reward for a match: Penalty for a mismatch:	
Use Mega BLAST Strand option Not Applicable	
Open gap 11 and extension gap 1 penalties gap x_dropoff 50 expect 10.0 word size 3 Filter 2 [Align]	
Sequence 1 Enter accession or GI CLONED E or download from file	
or sequence in FASTA format from: 0 to: 0 DIGNSFTESTULTHALSSQPMLSISEASUNQLKSULMDFSGLNVPHYGWQGLWSWGWAKTQ	
DPEPASSATITDPKKANRFHRTLLL/TWLPAGYVPSPKHRSPLIANTLWGNMLLATESLKNS	
AELTPSDHPFWGITGGGLGMMVYQEPRENHPGFHMRSSGYFAGMIAGQTHTPSLKFSQTYT KLNERYAKMNVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCHHFYTQGENLTSQGT	
FRSQTMGGAVFFDLFMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINV LVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHAMS	
YKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF	1
Sequence 2 Enter accession or GI CT8 MURD: or download from file	
or sequence in FASTA format from: 0 to: 0	<u>_</u>
NPASTTSDVAGLEXDPKD	P-17C+8
	P
	4
SAlign: (GleanImput)	」

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix BEOSEM62 gap open: 11 gap extension: 1 x_dropoff: 50 expect: 10.0 wordsize: 3 Filter Maligna

Sequence 1 Icl|seq_1 Length 955 PMPE ATCC PTA 2462 PTT CT3

Sequence 2 lcl|seq_2 Length 18 No significant similarity was found